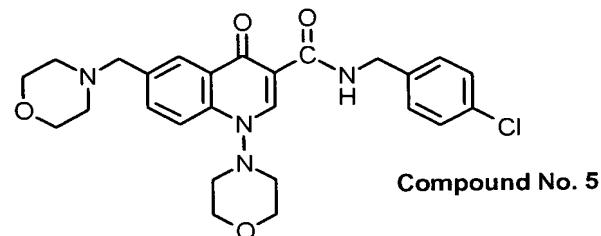
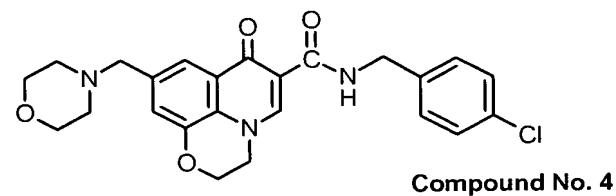
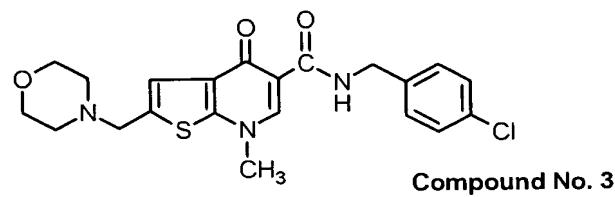
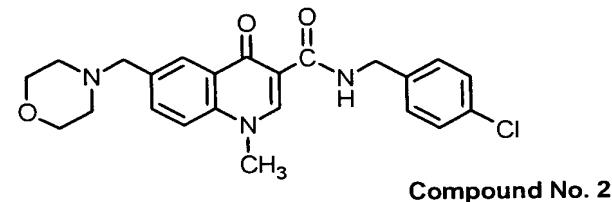
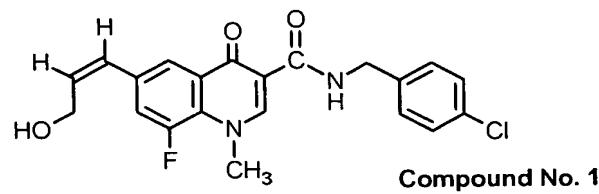
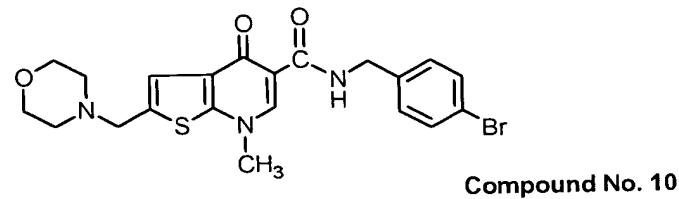
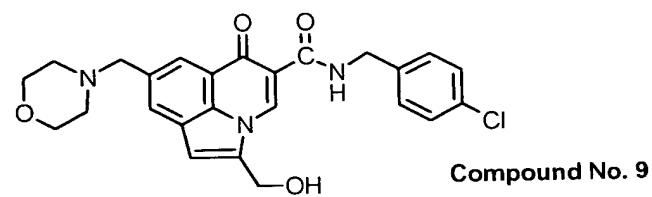
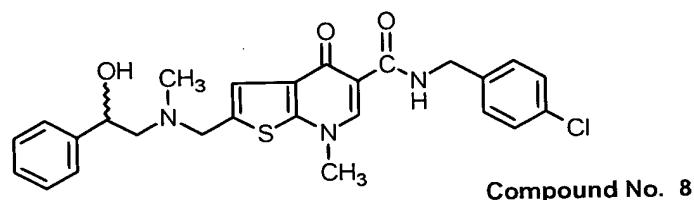
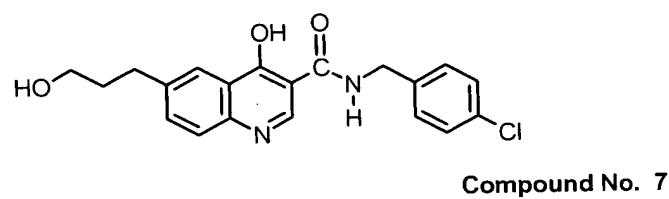
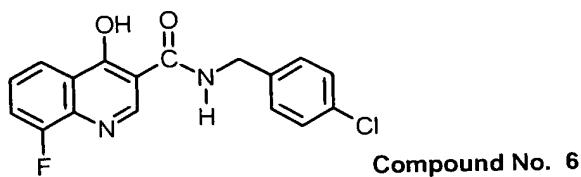
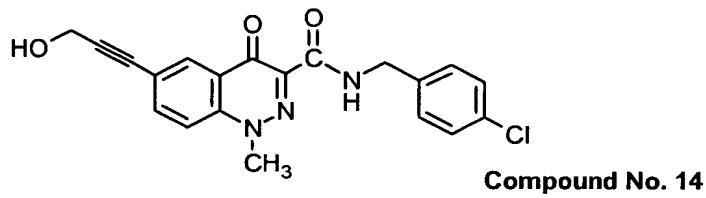
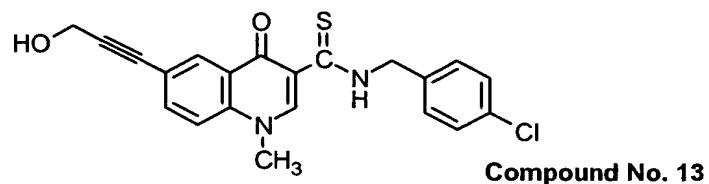
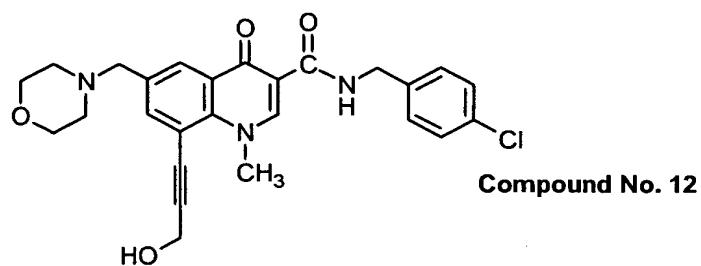
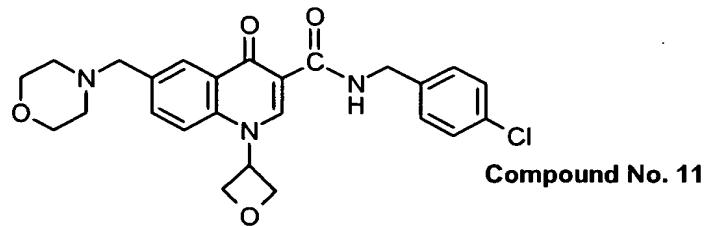


**Figure 1 4-HQ, 4-oxo-DHQ and 4-oxo-DHTP antiviral compounds**

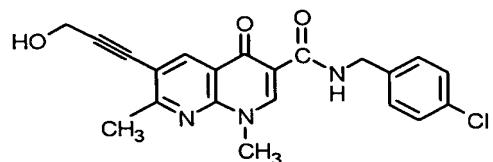
(Figure 1 continue)



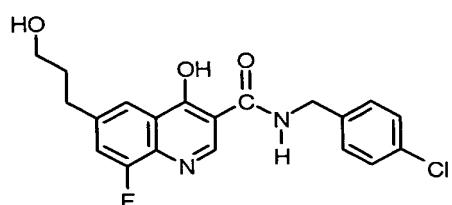
(Figure 1 continue)



**(Figure 1 continue)**

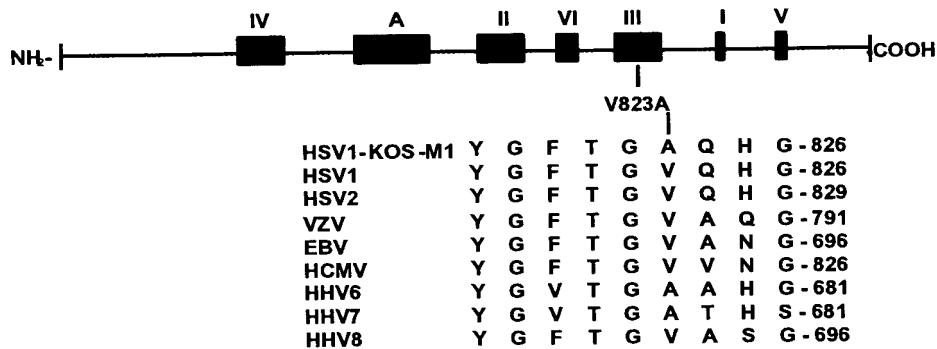


**Compound No.15**

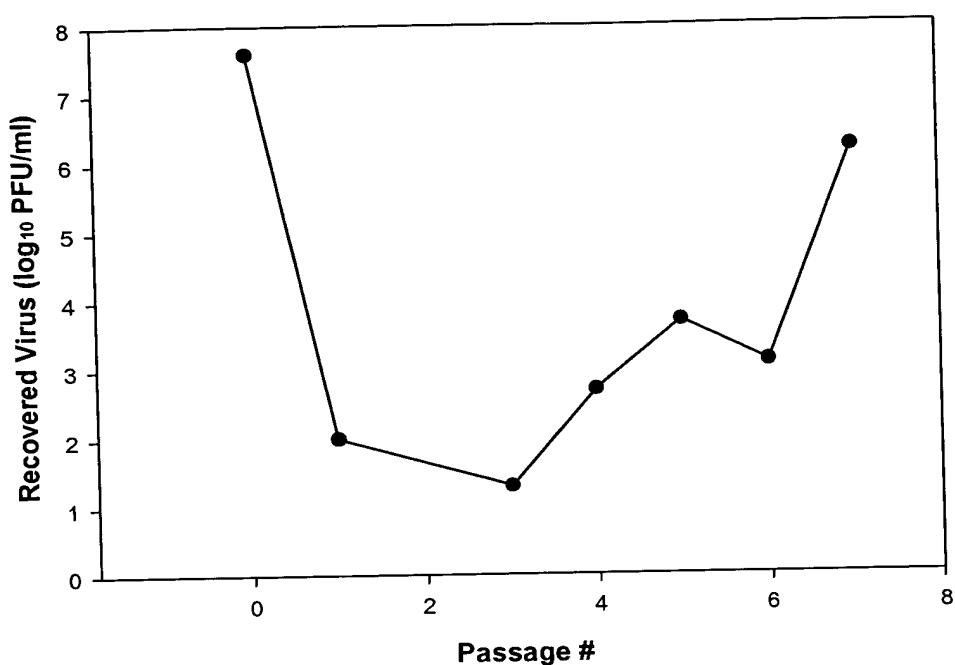


**Compound 17**

**Figure 2. The HSV1 (KOS Strain) DNA Polymerase Amino Acid 823 is Critical for Resistance to 4-Hydroxyquinolines and Related Compounds**



**Schematic of HSV1 polymerase illustrating the conserved regions A and I-VI found in class 2 polymerases. Also shown are the amino acid sequence for the highly conserved herpesvirus domain in region III which surrounds the HSV1 amino acid 823.**

**Figure 3      Serial Passage of HSV-1 in Presence of 20  $\mu$ M compound 17**

**Figure 4 Comparison of Wild type HSV-1 and HSV-2 DNA Polymerases Amino Acid Sequences Aligned by Amino Acid Homology\***

	HSV2-MS	MFCAAGGPTS	PGGKSAARAA	SGFFAPHNPR	GATQTAPPPC	RRQNFYNPHL	-50
	HSV2-186	MFCAAGGPAS	PGGKSAARAA	SGFFAPHNPR	GATQTAPPPC	RRQNFYNPHL	-50
5	HSV1-Kos	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
	HSV1-Patton	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
	HSV1-DJL	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
	HSV1-F	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
10	HSV2-MS	AQTGTQPKAP	GPAQRHTYY	ECDEFRFIAP	RSLDEDAPAE	QRTGVHDGRL	-100
	HSV2-186	AQTGTQPKAP	GPAQRHTYY	ECDEFRFIAP	RSLDEDAPAE	QRTGVHDGRL	-100
	HSV1-Kos	APVGTQQKPT	GPTQRHTYY	ECDEFRFIAP	RVLDEDAPPE	KRAGVHDGHL	-99
	HSV1-Patton	APVGTQQKPT	GPTQRHTYY	ECDEFRFIAP	RVLDEDAPPE	KRAGVHDGHL	-99
	HSV1-DJL	APVGTQQKPT	GPTQRHTYY	ECDEFRFIAP	RVLDEDAPPE	KRAGVHDGHL	-99
15	HSV1-F	APVGTQQKPT	GPTQRHTYY	ECDEFRFIAP	RVLDEDAPPE	KRAGVHDGHL	-99
	HSV2-MS	RRAPKVYCGG	DERDVLRVGP	EGFWPRLRL	WGGADHAPKG	FDPTVTVFHV	-150
	HSV2-186	RRAPKVYCGG	DERDVLRVGP	EGFWPRLRL	WGGADHAPEG	FDPTVTVFHV	-150
	HSV1-Kos	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRSL	WGGVDHAPAG	FNPTVTVFHV	-149
20	HSV1-Patton	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRSL	WGGVDHAPAG	FNPTVTVFHV	-149
	HSV1-DJL	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRSL	WGGVDHAPAG	FNPTVTVFHV	-149
	HSV1-F	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRSL	WGGVDHAPAG	FNPTVTVFHV	-149
	HSV2-MS	YDILEHVEHA	YSMRAAQLHE	RFMDAITPAG	TVITLLGLTP	EGHRVAHVHY	-200
25	HSV2-186	YDILEHVEHA	YSMRAAQLHE	RFMDAITPAG	TVITLLGLTP	EGHRVAHVHY	-200
	HSV1-Kos	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAHVHY	-199
	HSV1-Patton	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAHVHY	-199
	HSV1-DJL	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAHVHY	-199
	HSV1-F	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAHVHY	-199
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	HSV2-186	GTRQFYFMNK	AEVDRHLQCR	APRDLCERLA	AALRESPGAS	FRGISADHFE	-250
	HSV1-Kos	GTRQFYFMNK	EEVDRHLQCR	APRDLCERLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-Patton	GTRQFYFMNK	EEVDRHLQCR	APRDLCERLA	AALRESPGAS	FRGISADHFE	-249
35	HSV1-DJL	GTRQFYFMNK	EEVDRHLQCR	APRDLCERLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-F	GTRQFYFMNK	EEVDRHLQCR	APRDLCERLA	AALRESPGAS	FRGISADHFE	-249
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	HSV2-186	AEVVERADVY	YYETRPTLYY	RVFVRSGRAL	AYLCDNFCPA	IRKYEGGVDA	-300
40	HSV1-Kos	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCPA	IKKYEGGVDA	-299
	HSV1-Patton	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCPA	IKKYEGGVDA	-299
	HSV1-DJL	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCPA	IKKYEGGVDA	-299
	HSV1-F	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCPA	IKKYEGGVDA	-299
	HSV2-MS	TTRFILDNPG	FVTFGWYRLK	PGRGNAPAQP	RPPTAFTGTSS	DVEFNCTADN	-350
	HSV2-186	TTRFILDNPG	FVTFGWYRLK	PGRGNAPAQP	RPPTAFTGTSS	DVEFNCTADN	-350
	HSV1-Kos	TTRFILDNPG	FVTFGWYRLK	PGRNNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
	HSV1-Patton	TTRFILDNPG	FVTFGWYRLK	PGRNNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
45	HSV1-DJL	TTRFILDNPG	FVTFGWYRLK	PGRNNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
	HSV1-F	TTRFILDNPG	FVTFGWYRLK	PGRNNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
	HSV2-MS	LAVEGAMCDL	PAYKLMCFDI	ECKAGGEDEL	AFPVVAERPED	LVIQISCLLY	-400
	HSV2-186	LAVEGAMCDL	PAYKLMCFDI	ECKAGGEDEL	AFPVVAERPED	LVIQISCLLY	-400
	HSV1-Kos	LAIEGGMSDL	PAYKLMCFDI	ECKAGGEDEL	AFPVAGHPED	LVIQISCLLY	-399
55	HSV1-Patton	LAIEGGMSDL	PAYKLMCFDI	ECKAGGEDEL	AFPVAGHPED	LVIQISCLLY	-399
	HSV1-DJL	LAIEGGMSDL	PAYKLMCFDI	ECKAGGEDEL	AFPVAGHPED	LVIQISCLLY	-399
	HSV1-F	LAIEGGMSDL	PAYKLMCFDI	ECKAGGEDEL	AFPVAGHPED	LVIQISCLLY	-399
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	HSV2-186	DLSTTALEHI	LLFSLGSCDL	PESHLSLAS	RGLPAPVVLE	FDSEFEMLLA	-450
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	HSV1-Patton	DLSTTALEHV	LLFSLGSCDL	PESHNLNEAA	RGLPTPVVLE	FDSEFEMLLA	-449
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	HSV-Kos	FMTLVKQYGP	EFVTGYNIIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRGVF	-499
5	HSV1-Patton	FMTLVKQYGP	EFVTGYNIIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRGVF	-499
	HSV1-DJL	FMTLVKQYGP	EFVTGYNIIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRGVF	-499
	HSV1-F	FMTLVKQYGP	EFVTGYNIIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRGVF	-499
	HSV2-MS	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKVKLSSYK	LNAVAEAVLK	-550
10	HSV2-186	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKVKLSSYK	LNAVAEAVLK	-550
	HSV-Kos	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKIKLSSYK	LNAVAEAVLK	-549
	HSV1-Patton	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKIKLSSYK	LNAVAEAVLK	-549
	HSV1-DJL	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKIKLSSYK	LNAVAEAVLK	-549
	HSV1-F	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKIKLSSYK	LNAVAEAVLK	-549
15	HSV2-MS	DKKKDLSYRD	IPAYYASGPA	QRGVIGEYCV	QDSLLVGQLF	FKFLPHLELS	-600
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	HSV1-F	DKKKDLSYRD	IPAYYAAGPA	QRGVIGEYCI	QDSLLVGQLF	FKFLPHLELS	-599
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	HSV1-DJL	AVARLAGINI	TRTIYDGQQI	RVFTCLRLA	DQKGFFILPDT	QGRFRGAGGE	-649
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	HSV1-DJL	APKRPAARE	DEERP.....	EEEGEDENER	EEGGGEREPE	GARETAGRHV	-694
35	HSV1-F	APKRPAARE	DEERP.....	EEEGEDEDER	EEGGGEREPE	GARETAGRHV	-694
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55	HSV1-DJL	SSPEEAVLLD	KQQAAIKVVC	NSVYGFITGVQ	HGLLPCLHVA	ATVTTIGREM	-844
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	HSV1-Patton	LLATREYVHA	RWAEEFEQLLA	DFPEAADMRA	PGPYSMRIIY	GDTDSIFVLC	-894
	HSV1-DJL	LLATREYVHA	RWAEEFEQLLA	DFPEAADMRA	PGPYSMRIIY	GDTDSIFVLC	-894
	HSV1-F	LLATREYVHA	RWAEEFEQLLA	DFPEAADMRA	PGPYSMRIIY	GDTDSIFVLC	-894
65	HSV2-MS	RGLTAAGLVA	MGDKMASHIS	RALFLPPIKL	ECEKTFTKLL	LIAKKKYIGV	-947

	HSV2-186	RGLTAAGLVA MGDKMASHIS RALFLPPIKL ECEKTFTKLL LIAKKKYIGV -949
	HSV-Kos	RGLTAAGLTA MGDKMASHIS RALFLPPIKL ECEKTFTKLL LIAKKKYIGV -944
	HSV1-Patton	RGLTAAGLTA MGDKMASHIS RALFLPPIKL ECEKTFTKLL LIAKKKYIGV -944
	HSV1-DJL	RGLTAAGLTA VGDKMASHIS RALFLPPIKL ECEKTFTKLL LIAKKKYIGV -944
5	HSV1-F	RGLTAAGLTA VGDKMASHIS RALFLSPIKL ECEKTFTKLL LIAKKKYIGV -944
	HSV2-MS	I CGGKMLIKG VDLVRKNNCA FINRTSRALV DLLFYDDTVS GAAAALAERP -997
	HSV2-186	I CGGKMLIKG VDLVRKNNCA FINRTSRALV DLLFYDDTVS GAAAALAERP -999
	HSV-Kos	I YGGKMLIKG VDLVRKNNCA FINRTSRALV DLLFYDDTVS GAAAALAERP -994
10	HSV1-Patton	I YGGKMLIKG VDLVRKNNCA FINRTSRALV DLLFYDDTVS GAAAALAERP -994
	HSV1-DJL	I YGGKMLIKG VDLVRKNNCA FINRTSRALV DLLFYDDTVS GAAAALAERP -994
	HSV1-F	I YGGKMLIKG VDLVRKNNCA FINRTSRALV DLLFYDDTVS GAAAALAERP -994
	HSV2-MS	AEEWLARPLP EGLQAFGAVL VDAHRRITDP ERDIQDFVLT AELSRHPRAY -1047
15	HSV2-186	AEEWLARPLP EGLQAFGAVL VDAHRRITDP ERDIQDFVLT AELSRHPRAY -1049
	HSV-Kos	AEEWLARPLP EGLQAFGAVL VDAHRRITDP ERDIQDFVLT AELSRHPRAY -1044
	HSV1-Patton	AEEWLARPLP EGLQAFGAVL VDAHRRITDP ERDIQDFVLT AELSRHPRAY -1044
	HSV1-DJL	AEEWLARPLP EGLQAFGAVL VDAHRRITDP ERDIQDFVLT AELSRHPRAY -1044
	HSV1-F	AEEWLARPLP EGLQAFGAVL VDAHRRITDP ERDIQDFVLT AELSRHPRAY -1044
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	HSV2-186	TNKR LAHLTV YYKLMARRAQ VPSIKDRIPY VIVAQTREVE ETVARLAALR -1099
	HSV-Kos	TNKR LAHLTV YYKLMARRAQ VPSIKDRIPY VIVAQTREVE ETVARLAALR -1094
	HSV1-Patton	TNKR LAHLTV YYKLMARRAQ VPSIKDRIPY VIVAQTREVE ETVARLAALR -1094
25	HSV1-DJL	TNKR LAHLTV YYKLMARRAQ VPSIKDRIPY VIVAQTREVE ETVARLAALR -1094
	HSV1-F	TNKR LAHLTV YYKLMARRAQ VPSIKDRIPY VIVAQTREVE ETVARLAALR -1094
	HSV2-MS	ELDAAAPGDE PAPPAALPSP AKRPRETPSH ADPPGGASKP RKLLVSELAE -1147
	HSV2-186	ELDAAAPGDE PAPPAALPSP AKRPRETPSH ADPPGGASKP RKLLVSELAE -1149
30	HSV-Kos	ELDAAAPGDE PAPPAALPSP AKRPRETPSH ADPPGGASKP RKLLVSELAE -1144
	HSV1-Patton	ELDAAAPGDE PAPPAALPSP AKRPRETPSP ADPPGGASKP RKLLVSELAE -1144
	HSV1-DJL	ELDAAAPGDE PAPPAALPSP AKRPRETPSP ADPPGGASKP RKLLVSELAE -1144
	HSV1-F	ELDAAAPGDE PAPPAALPSP AKRPRETPSH ADPPCGASKP RKLLVSELAE -1144
	HSV2-MS	DPGYAIARGV PLNTDYYFSH LLGAACVTFK ALFGNNAKIT ESLLKRFIPE -1197
	HSV2-186	DPGYAIARGV PLNTDYYFSH LLGAACVTFK ALFGNNAKIT ESLLKRFIPE -1199
	HSV-Kos	DPAYAIAHGV ALNTDYYFSH LLGAACVTFK ALFGNNAKIT ESLLKRFIPE -1194
	HSV1-Patton	DPAYAIAHGV ALNTDYYFSH LLGAACVTFK ALFGNNAKIT ESLLKRFIPE -1194
	HSV1-DJL	DPAYAIAHGV ALNTDYYFSH LLGAACVTFK ALFGNNAKIT ESLLKRFIPE -1194
40	HSV1-F	DPAYAIAHGV ALNTDYYFSH LLGAACVTFK ALFGNNAKIT ESLLKRFIPE -1194
	HSV2-MS	TWHPPDDVAA RLRAAGFGPA GAGATAEETR RMLHRAFDTL A* -1238
	HSV2-186	TWHPPDDVAA RLRAAGFGPA GAGATAEETR RMLHRAFDTL A* -1240
	HSV-Kos	VWHPPDDVAA RLRAAGFGAV GAGATAEETR RMLHRAFDTL A* -1235
45	HSV1-Patton	VWHPPDDVTA RLRAAGFGAV GAGATAEETR RMLHRAFDTL A* -1235
	HSV1-DJL	VWHPPDDVAA RLRTAGFGAV GAGATAEETR RMLHRAFDTL A* -1235
	HSV1-F	VWHPPDDVAA RLRAAGFGAV GAGATAEETR RMLHRAFDTL A* -1235

\*Amino acid alignment demonstrates difference in amino acid's sequences.

50 \*The gaps “....” indicate missing amino acids relative to other strains.

\*Wild HSV2-MS is listed as SEQ. ID NO 14.

\*Wild HSV2-186 is listed as SEQ. ID NO 15.

\*Wild HSV-Kos is listed as SEQ. ID NO 16.

\*Wild HSV1-Patton is listed as SEQ. ID NO 17.

55 \*Wild HSV1-DJL is listed as SEQ. ID NO 18.

\*Wild HSV1-F is listed as SEQ. ID NO 19.

**Figure 5 DNA and amino acid sequence list**

**SEQ. ID. NO. 1** DNA sequence of DNA polymerase gene for HSV2-MS-M1

5           1 ATGTTTGTG CCGCGGGCGG CCCGACTTCC CCCGGGGGGA AGTCGGCGGC  
       51 TCGGGCGGCG TCTGGGTTT TTGCCCCCA CAACCCCCGG GGAGGCCACCC  
 10       101 AGACGGCACC GCCGCCTTGC CGCCGGCAGA ACTTCTACAA CCCCCACCTC  
       151 GCTCAGACCG GAACGCAGCC AAAGGCCCCC GGGCCGGCTC AGGCCATAC  
       201 GTACTACAGC GAGTGCACG AATTTCGATT TATCGCCCCG CGTCGCTGG  
 15       251 ACGAGGACGC CCCCAGGGAG CAGCGCACCG GGGTCCACGA CGGCCGCCTC  
       301 CGGCGCGCCC CTAAGGTGTA CTGCGGGGG GACGAGCGCG ACGTCCTCCG  
 20       351 CGTGGGCCCG GAGGGCTTCT GGCCGCGTCG CTTGCGCCTG TGGGGCGGTG  
       401 CGGACCATGC CCCCAAGGGG TTCGACCCCA CCGTCACCGT CTTCCACGTG  
       451 TACGACATCC TGGAGCACGT GGAACACCGC TACAGCATGC GCGCCGCCA  
 25       501 GCTCCACGAG CGATTATGG ACGCCATCAC GCCCAGGGG ACCGTATCA  
       551 CGCTTCTGGG TCTGACCCCC GAAGGCCATC GCGTCGCCGT TCACGTCTAC  
 30       601 GGCACCGGGC AGTACTTTA CATGAACAAG GCGGAGGTGG ATCGGCACCT  
       651 GCAGTGCCGT GCCCCCGCG ATCTCTGCGA GCGCCTGGCG GCGGCCCTGC  
       701 GCGAGTCGCC GGGGGCGTCG TTCCGCGGA TCTCCGCGGA CCACCTCGAG  
 35       751 GCGGAGGTGG TGGAGCGCGC CGACGTGTAC TATTACGAAA CGCGCCCGAC  
       801 CCTGTACTAC CGCGTCTTCG TCGAAGCGG GCGCGCGCTG GCCTACCTGT  
 40       851 GCGACAACCT TTGCCCCCG ATCAGGAAGT ACGAGGGGG CGTCGACGCC  
       901 ACCACCCGGT TTATCCTGGA CAACCCGGGG TTTGTCACCT TCGGCTGGTA  
       951 CCGCCTCAAG CCCGGCCGCG GGAACCGGCC GGCCCAACCG CGCCCCCGA  
 45       1001 CGCGTTCGG AACCTCGAGC GACGTGAGT TTAAC TGAC GCGGACAAC  
       1051 CTGGCCGTCG AGGGGGCCAT GTGTGACCTG CGGCCTACA AGCTCATGTG  
 50       1101 CTTCGATATC GAATGCAAGG CCGGGGGGGA GGACGAGCTG GCCTTCCGG  
       1151 TCGCGGAACG CCCGGAAGAC CTCGTACATCC AGATCTCCTG TCTGCTCTAC  
       1201 GACCTGTCCA CCACCGCCCT CGAGCACATC CTCCTGTTT CGCTCGGATC  
 55       1251 CTGCGACCTC CCCGAGTCCC ACCTCAGCGA TCTCGCCTCC AGGGGCCTGC

1301 CGGCCCGT CGTCCTGGAG TTTGACAGCG AATTCGAGAT GCTGCTGGCC  
 1351 TTCATGACCT TCGTCAAGCA GTACGGCCCC GAGTCGTGA CCGGGTACAA  
 5 1401 CATCATCAAC TTGACTGGC CCTTCGTCC GACCAAGCTG ACGGAGATCT  
 1451 ACAAGGTCCC GCTCGACGGG TACGGGCGCA TGAACGGCCG GGGTGTGTC  
 1501 CGCGTGTGGG ACATCGGCCA GAGCCACTT CAGAACGCGA GCAAGATCAA  
 10 1551 GGTGAACGGG ATGGTGAACA TCGACATGTA CGGCATCATC ACCGACAAGG  
 1601 TCAAACCTCTC CAGCTACAAG CTGAACGCCG TCGCCGAGGC CGTCTTGAAG  
 15 1651 GACAAGAAGA AGGATCTGAG CTACCGCGAC ATCCCCGCCT ACTACGCCCTC  
 1701 CGGGCCCGCG CAGCGCGGG TGATCGGCGA GTATTGTGTG CAGGACTCGC  
 1751 TGCTGGTCGG GCAGCTGTT TCAGTTTGAC TTCAAGTTTC TGCCGCACCT GGAGCTTCC  
 20 1801 GCCGTCGCGC GCCTGGCGGG CATCAACATC ACCCGCACCA TCTACGACGG  
 1851 CCAGCAGATC CGCGTCTTCA CGTGCCTCCT GCGCCTGCG GGCCAGAAGG  
 25 1901 GCTTCATCCT GCCGGACACC CAGGGGCGGT TTCGGGGCCT CGACAAGGAG  
 1951 GCGCCAAGC GCCCGGCCGT GCCTGGGGGG GAAGGGGAGC GGCCGGGGGA  
 2001 CGGGAACGGG GACGAGGATA AGGACGACGA CGAGGACGAG GACGGGGACG  
 30 2051 AGCGCGAGGA GGTCGCGCGC GAGACCGGGG GCCGGCACGT TGGGTACCAG  
 2101 GGGGCCGGG TCCTCGACCC CACCTCCGGG TTTCACGTCG ACCCCGTGGT  
 35 2151 GGTGTTGAC TTTGCCAGCC TGTACCCAG CATCATCCAG GCCCACAAACC  
 2201 TGTGCTTCAG TACGCTCTCC CTGCGGCCCG AGGCCGTCGC GCACCTGGAG  
 2251 CGGGACCGGG ACTACCTGGA GATCGAGGTG GGGGGCCGAC GGCTGTTCTT  
 40 2301 CGTGAAGGCC CACGTACGCG AGAGCCTGCT GAGCATCCTG CTGCGCGACT  
 2351 GGCTGGCCAT GCGAAAGCAG ATCCGCTCGC GGATCCCCCA GAGCACCCCC  
 45 2401 GAGGAGGCCG TCCTCCTCGA CAAGCAACAG GCCGCCATCA AGGTGGTGTG  
 2451 CAACTCGGTG TACGGGTTCA CCGGGGCGCA GCACGGTCTT CTGCCCTGCC  
 2501 TGCACGTGGC CGCCACCGTG ACGACCATCG GCCGCGAGAT GCTCCTCGCG  
 50 2551 ACGCGCGCGT ACGTGCACGC GCGCTGGCG GAGTCGATC AGCTGCTGGC  
 2601 CGACTTCCG GAGGCGGCCG GCATGCGCGC CCCCGGTCCG TACTCCATGC  
 55 2651 GCATCATCTA CGGGGACACG GACTCCATT TCGTTTGTG CCGCGGCCTC  
 2701 ACGGCCCGCG GCCTGGTGGC CATGGGCGAC AAGATGGCGA GCCACATCTC  
 2751 GCGCGCGCTG TTCCCTCCCCC CGATCAAGCT CGAGTGCAGAA AAAACGTTCA

2801 CCAAGCTGCT GCTCATCGCC AAGAAAAAGT ACATCGGCGT CATCTGCAGG  
2851 GGCAAGATGC TCATCAAGGG CGTGGATCTG GTGCGAAAA ACAACTGCGC  
5 2901 GTTTATCAAC CGCACCTCCA GGGCCCTGGT CGACCTGCTG TTTTACGACG  
2951 ATACCGTATC CGGAGCGGCC GCCGCGTTAG CCGAGCGCCC CGCAGAGGAG  
10 3001 TGGCTGGCGC GACCCCTGCC CGAGGGACTG CAGGCCTTCG GGGCCGTCC  
3051 CGTAGACGCC CATCGCGCA TCACCGACCC GGAGAGGGAC ATCCAGGACT  
15 3101 TTGTCCCTCAC CGCCGAACCTG AGCAGACACC CGCGCGCGTA CACCAACAAG  
3151 CGCCTGGCCC ACCTGACGGT GTATTACAAG CTCATGGCCC GCCGCGCGCA  
3201 GGTCCCCGTCC ATCAAGGACC GGATCCCGTA CGTGATCGT GCCCAGACCC  
20 3251 GCGAGGTTAGA GGAGACGGTC GCGCGGCTGG CCGCCCTCCG CGAGCTAGAC  
3301 GCCGCCGCC CAGGGGACGA GCCCGCCCCC CCAGCGGCC TGCCCTCCCC  
3351 GGCCAAGCGC CCCCGGGAGA CGCCGTCGCA TGCCGACCCC CCAGGGAGGCG  
25 3401 CGTCCAAGGCC CCGCAAGCTG CTGGTGTCCG AGCTGGCGGA GGATCCCGGG  
3451 TACGCCATCG CCCGGGGCGT TCCGCTAAC ACGGACTATT ACTTCTCGCA  
30 3501 CCTGCTGGGG GCGGCCTGCG TGACGTTCAA GGCCCTGTT GGAAATAACG  
3551 CCAAGATCAC CGAGAGTCTG TTAAAGAGGT TTATTCCGA GACGTGGCAC  
3601 CCCCCGGACG ACGTGGCCGC GCGGCTCAGG GCCGCGGGGT TCGGGCCGGC  
35 3651 GGGGGCCGGC GCTACGGCGG AGGAAACTCG TCGAATGTTG CATAGAGCCT  
3701 TTGATACTCT AGCATGA

**SEQ. ID. NO. 2** Amino acid sequence of DNA polymerase for HSV2-MS-M1

1 MFCAAGGPTS PGGKSAARAA SGFFAPHNPR GATQTAPPPC RRQNFYNPHL  
 5 51 AQTGTQPKAP GPAQRHTYYS ECDEFRFLAP RSLDEDAPAE QRTGVHDGRL  
 10 101 RRAPKVYCGG DERDVLRVGP EGFWPRLRL WGGADHAPKG FDPTVTVFHV  
 15 151 YDILEHVEHA YSMRAAQLHE RFMDAITPAG TVITLLGLTP EGHRVAVHVY  
 20 201 GTRQYFYMNK AEVDRHLQCR APRDLCERLA AALRESPGAS FRGISADHFE  
 25 251 AEVVERADVY YYETRPTLYY RVFVRSGRAL AYLCDNFCPA IRKYEGGVDA  
 30 301 TTRFIELDNPG FVTFGWYRLK PGRGNAPAQP RPPTAFTSS DVEFNCTADN  
 35 351 LAVEGAMCDL PAYKLMCFDI ECKAGGEDEL AFPVAERPED LVIQISCLLY  
 40 401 DLSTTALEHI LLFSLGSCDL PESHLSDLAS RGLPAPVVLE FDSEFEMLLA  
 45 451 FMTFVKQYGP EFVTGYNIIN FDWPFWLTKL TEIYKVPLDG YGRMNGRGVF  
 50 501 RVWDIGQSHF QKRSKIKVNG MVNIDMYGII TDKVKLSSYK LNAVAEAVLK  
 55 551 DKKKDLDSYRD IPAYYASGPA QRGVIGEYCV QDSLLVGQLF FKFLPHLELS  
 60 601 AVARLAGINI TRTIYDGQQI RVFTCLLRLA GQKGFLPDT QGRFRGLDKE  
 65 651 APKRPAPVRG EGERPGDGNG DEDKDDDEDE DGDEREEVAR ETGGRHVGYQ  
 70 701 GARVLDPTSG FHVDPPVVFD FASLYPSIIQ AHNLCFSTLS LRPEAVAHLE  
 75 751 ADRDYLEIEV GGRRLLFFVKA HVRESLLSIL LRDWLAMRKQ IRSRIPQSTP  
 80 801 EEAVALDKQQ AAIKVVCNSV YGFTGAQHGL LPCLHVAATV TTIGREMLLA  
 85 851 TRAYVHARWA EFDQLLADFP EAAGMRAPGP YSMRIIYGDT DSIFVLCRGL  
 90 901 TAAGLVAMGD KMASHISRAL FLPPIKLECE KTFTKLLLIA KKKYIGVICG  
 95 951 GKMLIKGVDL VRKNNCAFIN RTSRALVDLL FYDDTVSGAA AALAERPAEE  
 100 1001 WLARPLPEGL QAFGAVLVDA HRRITDPERD IQDFVLTAEL SRHPRAYTNK  
 105 1051 RLAHLTVYYK LMARRAQVPS IKDRIPYVIV AQTREVEETV ARLAALRELD  
 110 1101 AAAPGDEPAP PAALPSPAKR PRETPSHADP PGGASKPRKL LVSELAEDPG  
 115 1151 YAIARGVPLN TDYYFSHLLG AACVTFKALF GNNAKITESL LKRFIPETWH  
 120 1201 PPDDVAARLR AAGFGPAGAG ATAEEETRRML HRAFDTLA\*

**SEQ.ID.NO. 3** DNA sequence of DNA polymerase gene for HSV2-186-M1

1 ATGTTTGTG CCGCGGGCGG CCCGGCTTCC CCCGGGGGGA AGTCGGCGGC  
 5 51 TCGGGCGGCG TCTGGGTTTT TTGCCCCCCA CAACCCCCGG GGAGGCCACCC  
 10 101 AGACGGCACC GCCGCCTTGC CGCCGGCAGA ACTTCTACAA CCCCCCACCTC  
 15 151 GCTCAGACCG GAACGCAGCC AAAGGCCCCC GGGCCGGCTC AGGCCATAC  
 20 201 GTACTACAGC GAGTGCAGC AATTTCGATT TATCGCCCCG CGTCGCTGG  
 25 251 ACGAGGACGC CCCCGCGGAG CAGCGCACCG GGGTCCACGA CGGCCGCCTC  
 30 301 CGGCGCGCCC CTAAGGTGTA CTGCGGGGGG GACGAGCGCG ACGTCCTCCG  
 35 351 CGTGGGCCCG GAGGGCTTCT GGCGCGTCTG CTTGCGCCTG TGGGGCGGTG  
 40 401 CGGACCATGC CCCCGAGGGG TTCGACCCCA CCGTCACCGT CTTCCACGTG  
 45 451 TACGACATCC TGGAGCACGT GGAACACGCG TACAGCATGC GCGCCGCCA  
 50 501 GCTCCACGAG CGATTATGG ACGCCATCAC GCCCCCGGG ACCGTCATCA  
 55 551 CGCTTCTGGG TCTGACCCCC GAAGGCCATC GCGTCGCCGT TCACGTCTAC  
 60 601 GGCACCGGGC AGTACTTTA CATGAACAAG GCGGAGGTGG ATCGGCACCT  
 65 651 GCAGTGCCGT GCCCGCGCG ATCTCTGCGA GCGCCTGGCG GCGGCCCTGC  
 70 701 GCGAGTCGCC GGGGGCGTCG TTCCGCGGCA TCTCCGCGGA CCACTCGAG  
 75 751 GCGGAGGTGG TGGAGCGCGC CGACGTGTAC TATTACGAAA CGCGCCGAC  
 80 801 CCTGTACTAC CGCGTCTTCG TGCGAAGCGG GCGCGCGCTG GCCTACCTGT  
 85 851 GCGACAACCTT TTGCCCCCGG ATCAGGAAGT ACGAGGGGGG CGTCGACGCC  
 90 901 ACCACCCGGT TTATCCTGGA CAACCCGGGG TTTGTCACCT TCGGCTGGTA  
 95 951 CCGCCTCAAG CCCGGCCCGG GGAACCGCGC GGCCCAACCG CGCCCCCGA  
 100 1001 CGGCGTTCGG AACCTCGAGC GACGTGAGT TTAACTGCAC GGCGGACAAC  
 105 1051 CTGGCCGTG AGGGGGCCAT GTGTGACCTG CCGGCCTACA AGCTCATGTG  
 110 1101 CTTCGATATC GAATGCAAGG CCGGGGGGGG GGACGAGCTG GCCTTCCGG  
 115 1151 TCGCGGAACG CCCGGAAGAC CTCGTCATCC AGATCTCCTG TCTGCTCTAC  
 120 1201 GACCTGTCCA CCACCGCCCT CGAGCACATC CTCCGTGTTT CGCTCGGATC  
 125 1251 CTGCGACCTC CCCGAGTCCC ACCTCAGCGA TCTCGCCTCC AGGGGCCTGC  
 130 1301 CGGCCCCCGT CGTCCTGGAG TTTGACAGCG AATTGAGAT GCTGCTGGCC  
 135 1351 TTCATGACCT TCGTCAAGCA GTACGGCCCC GAGTCGTGA CGGGGTACAA  
 140 1401 CATCATCAAC TTCGACTGGC CCTTCGTCC GACCAAGCTG ACGGAGATCT

1451 ACAAGGTCCC GCTCGACGGG TACGGGCGCA TGAACGGCCG GGGTGTGTT  
 1501 CGCGTGTGGG ACATCGGCCA GAGCCACTT CAGAACGCA GCAAGATCAA  
 5 1551 GGTGAACGGG ATGGTGAACA TCGACATGTA CGGCATCATC ACCGACAAGG  
 1601 TCAAACCTCTC CAGCTACAAG CTGAACGCCG TCGCCGAGGC CGTCTTGAAG  
 10 1651 GACAAGAAGA AGGATCTGAG CTACCGCGAC ATCCCCGCCT ACTACGCCCTC  
 1701 CGGGCCCGCG CAGCGCGGGG TGATCGCGA GTATTGTGTG CAGGACTCGC  
 1751 TGCTGGTCGG GCAGCTGTT TCAGTTC TTCAAGTTTC TGCCGCACCT GGAGCTTCC  
 15 1801 GCCGTCGCGC GCCTGGCGGG CATCAACATC ACCCGCACCA TCTACGACGG  
 1851 CCAGCAGATC CGCGTCTTCA CGTGCCTCCT GCGCCTGCG GGCCAGAAGG  
 20 1901 GCTTCATCCT GCCGGACACC CAGGGCGGT TTCGGGGCCT CGACAAGGAG  
 1951 GCGCCAAGC GCCCGGCCGT GCCTCGGGGG GAAGGGGAGC GGCGGGGGGA  
 2001 CGGGAACGGG GACGAGGATA AGGACGACGA CGAGGACGGG GACGAGGACG  
 25 2051 GGGACGAGCG CGAGGAGGTC GCGCGCGAGA CCGGGGGCCG GCACGTTGGG  
 2101 TACCAGGGGG CCCGGGTCTT CGACCCCACC TCCGGGTTTC ACGTCGACCC  
 30 2151 CGTGGTGGTG TTTGACTTTG CCAGCCTGTA CCCCAGCATC ATCCAGGCC  
 2201 ACAACCTGTG CTTCAGTACG CTCTCCCTGC GGCCCGAGGC CGTCGCGCAC  
 2251 CTGGAGGCGG ACCGGGACTA CCTGGAGATC GAGGTGGGGG GCCGACGGCT  
 35 2301 GTTCTTCGTG AAGGCCACG TACGCGAGAG CCTGCTGAGC ATCCTGCTGC  
 2351 GCGACTGGCT GGCCATGCGA AAGCAGATCC GCTCGCGGAT CCCCCAGAGC  
 40 2401 CCCCCCGAGG AGGCCGTCTT CCTCGACAAG CAACAGGCCG CCATCAAGGT  
 2451 GGTGTGCAAC TCGGTGTACG GGTTCACCGG GGCGCAGCAC GGTCTTCTGC  
 2501 CCTGCCTGCA CGTGGCCGCC ACCGTGACGA CCATCGGCCG CGAGATGCTC  
 45 2551 CTCGCGACGC GCGCGTACGT GCACGCGCGC TGGGCGGAGT TCGATCAGCT  
 2601 GCTGGCCGAC TTTCCGGAGG CGGCCGGCAT GCGCGCCCCC GGTCCGTACT  
 50 2651 CCATGCGCAT CATCTACGGG GACACGGACT CCATTTCTGT TTTGTGCCGC  
 2701 GGCCTCACGG CCGCGGGCCT GGTGGCCATG GGCGACAAGA TGGCGAGCCA  
 2751 CATCTCGCGC GCGCTGTTCC TCCCCCGAT CAAGCTCGAG TGCGAAAAAA  
 55 2801 CGTTCACCAA GCTGCTGCTC ATCGCCAAGA AAAAGTACAT CGGCGTCATC  
 2851 TGCGGGGCA AGATGCTCAT CAAGGGCGTG GATCTGGTGC GCAAAAACAA

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2901 CTGCGCGTTT ATCAACCGCA CCTCCAGGGC CCTGGTCGAC CTGCTGTTT  
2951 ACGACGATAC CGTATCCGGA GCGGCCGCCG CGTTAGCCGA GCGCCCCGCA  
5 3001 GAGGAGTGGC TGGCGCGACC CCTGCCGAG GGACTGCAGG CGTCGGGGC  
3051 CGTCCTCGTA GACGCCATC GGCGCATCAC CGACCCGGAG AGGGACATCC  
3101 AGGACTTTGT CCTCACCGCC GAACTGAGCA GACACCCGCG CGCGTACACC  
10 3151 AACAAAGCGCC TGGCCCACCT GACGGTGTAT TACAAGCTCA TGGCCCGCCG  
3201 CGCGCAGGTC CCGTCCATCA AGGACCGGAT CCCGTACGTG ATCGTGGCCC  
15 3251 AGACCCGCGA GGTAGAGGAG ACGGTCGCGC GGCTGGCCGC CCTCCCGAG  
3301 CTAGACGCGG CCGCCCCAGG GGACGAGCCC GCCCCCCCAG CGGCCCTGCC  
3351 CTCCCCGGCC AAGCGCCCCC GGGAGACGCC GTCGCATGCC GACCCCCCGG  
20 3401 GAGGCGCGTC CAAGCCCCGC AAGCTGCTGG TGTCCGAGCT GGCGGAGGAT  
3451 CCCGGGTACG CCATCGCCCG GGGCGTTCCG CTCAACACGG ACTATTACTT  
3501 CTCGCACCTG CTGGGGCGG CCTGCGTGAC GTTCAAGGCC CTGTTGGAA  
3551 ATAACGCCAA GATCACCGAG AGTCTGTTAA AGAGGTTAT TCCCGAGACG  
3601 TGGCACCCCC CGGACGACGT GGCGCGCGG CTCAGGGCCG CGGGGTTCGG  
30 3651 GCCGGCGGGG GCCGGCGCTA CGGCGGAGGA AACCTCGTCGA ATGTTGCATA  
3701 GAGCCTTGA TACTCTAGCA TGA

35

**SEQ.ID.NO. 4 Amino acid sequence of DNA polymerase for HSV2-186-M1**

5        1 MFCAAGGPAS PGGKSAARAA SGFFAPHNPR GATQTAPPPC RRQNFYNPHL  
 51      51 AQTGTQPKAP GPAQRHTYYS ECDEFRFIAP RSLDEDAPAE QRTGVHDGRL  
 101     101 RRAPKVYCGG DERDVLRVGP EGFWPRLRL WGGADHAPEG FDPTVTVFHV  
 10      151 YDILEHVEHA YSMRAAQLHE RFMDAITPAG TVITLLGLTP EGHRVAVHVY  
 201     201 GTRQYFYMNK AEVDRHLQCR APRDLCERLA AALRESPGAS FRGISADHFE  
 15      251 AEVVERADVY YYETRPTLYY RVFVRSGRAL AYLCDNFCPA IRKYEGGVDA  
 301     301 TTRFILDNPNG FVTFGWYRLK PGRGNAPAQP RPPTAFTSS DVEFNCTADN  
 20      351 LAVEGAMCDL PAYKLMCFDI ECKAGGEDEL AFPVAERPED LVIQISCLLY  
 401     401 DLSTTALEHI LLFSLGSCDL PESHLSDLAS RGLPAPVVLE FDSEFEMILLA  
 451     451 FMTFKVKQYGP EFVTGYNIIN FDWPFVLTKL TEIYKVPLDG YGRMNGRGVF  
 25      501 RVWDIGQSHF QKRSKIKVNG MVNIDMYGII TDKVKLSSYK LNAVAEAVLK  
 551     551 DKKKDLSYRD IPAYYASGPA QRGVIGEYCV QDSLLVGQLF FKFLPHLELS  
 601     601 AVARLAGINI TRTIYDGQQI RVFTCLLRLA GQKGFILPDT QGRFRGLDKE  
 30      651 APKRPAPVRG EGERPGDGNG DEDKDDDEDG DEDGDEREV ARETGGRHVG  
 701     701 YQGARVLDPT SGFHVDPVVV FDFASLYPSI IQAHNLCFST LSLRPEAVAH  
 35      751 LEADRDXLEI EVGGRRLLFFV KAHVRESLLS ILLRDWLAMR KQIRSRIQS  
 801     801 PPEEAVIDDK QQAAIKVVCN SVYGFTGAQH GLLPCLHVAA TVTTIGREML  
 40      851 LATRAYVHAR WAEFDQLLAD FPEAAGMRAP GPYSMRIIYG DTDSIFVLCR  
 901     901 GLTAAGLVAM GDKMASHISR ALFLPPIKLE CEKTFTKLLL IAKKKYIGVI  
 951     951 CGGKMLIKGV DLVRKNNCAF INRTSRALVD LLFYDDTVSG AAAALAERPA  
 45      1001 EEWLARPLPE GLQAFGAVLV DAHRRITDPE RDIQDFVLTA ELSRHPRAYT  
 1051    1051 NKRLAHLTVY YKLMARRAQV PSIKDRIPYV IVAQTREVEE TVARLAALRE  
 1101    1101 LDAAAPGDEP APPAALPSPA KRPRETPSHA DPPGGASKPR KLLVSELAED  
 50      1151 PGYAIARGVP LNTDYYFSHL LGAACVTFKA LFGNNAKITE SLLKRFIPET  
 1201    1201 WHPPDDVAAR LRAAGFGPAG AGATAEETRR MLHRAFDTLA \*  
 55

**SEQ.ID.NO. 5** DNA sequence of DNA polymerase gene for HSV1-KOS-M1

1 ATGTTTCCG GTGGCGGCCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC  
 5 51 CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC  
 10 101 GGGGACCCCC GCCTGTTTG AGGCAAAACT TTTACAACCC CTACCTCGCC  
 151 CCAGTCGGGA CGAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA  
 10 201 CTATAGCGAA TGCGATGAAT TTCGATTAT CGCCCCGCGG GTGCTGGACG  
 251 AGGATGCCCG CCCGGAGAAG CGCGCCGGGG TGACAGACGG TCACCTCAAG  
 15 301 CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCCTCCGCGT  
 351 CGGGTCGGGC GGCTCTGGC CGCGCGCTC GCGCCTGTGG GGCGGCGTGG  
 401 ACCACGCCCGG GGCGGGGTTTC AACCCCACCG TCACCGTCTT TCACGTGTAC  
 20 451 GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCAGTT  
 501 CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC  
 25 551 TCCTGGGCCT GACTCCGGAA GGCCACCGGG TGGCCGTTCA CGTTTACGGC  
 601 ACGCGGCAGT ACTTTACAT GAACAAGGAG GAGGTTGACA GGCACCTACA  
 651 ATGCCGCGCC CCACGAGATC TCTGCGAGCG CATGCCGCG GCCCTGCGCG  
 30 701 AGTCCCCGGG CGCGTCGTTTC CGCGGCATCT CCGCGGACCA CTTCGAGGCG  
 751 GAGGTGGTGG AGCGCACCGA CGTGTACTAC TACGAGACGC GCCCCGCTCT  
 35 801 GTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTCG TACCTGTGCG  
 851 ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC  
 901 ACCCGGTTCA TCCTGGACAA CCCCGGGTTTC GTCACCTTCG GCTGGTACCG  
 40 951 TCTCAAACCG GGCGGAACA ACACGCTAGC CCAGCGCGG GCCCCGATGG  
 1001 CCTTCGGGAC ATCCAGCGAC GTCGAGTTA ACTGTACGGC GGACAACCTG  
 45 1051 GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT  
 1101 CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG  
 1151 CGGGGCACCC GGAGGACCTG GTTATTCAAGA TATCCTGTCT GCTCTACGAC  
 50 1201 CTGTCCACCA CCGCCCTGGA GCACGTCCTC CTGTTTCGC TCGGTTCTG  
 1251 CGACCTCCCC GAATCCCACC TGAACGAGCT GGCGGCCAGG GGCCTGCCA  
 55 1301 CGCCCGTGGT TCTGGAATTG GACAGCGAAT TCGAGATGCT GTTGGCCTTC  
 1351 ATGACCCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT  
 1401 CATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGTTGACG GACATTACA

1451 AGGTCCCCCT GGACGGGTAC GGCCGCATGA ACGGCCGGGG CGTGTTCGC  
 1501 GTGTGGGACA TAGGCCAGAG CCACCTCCAG AAGCGCAGCA AGATAAAGGT  
 5 1551 GAACGGCATG GTAACATCG ACATGTACGG GATCATAACC GACAAGATCA  
 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC  
 10 1651 AAGAAGAAGG ACCTGAGCTA TCGCGACATC CCCGCCTACT ACGCCGCCGG  
 1701 GCCCGCGCAA CGCGGGGTGA TCGCGAGTA CTGCATACAG GATTCCCTGC  
 1751 TGGTGGGCCA GCTGTTTTT AAGTTTTGC CCCATCTGGA GCTCTCGGCC  
 15 1801 GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA  
 1851 GCAGATCCGC GTCTTACGT GCCTGCTGCG CCTGGCCGAC CAGAAGGGCT  
 20 1901 TTATTCTGCC GGACACCCAG GGGCGATTAA GGGCGCCGG GGGGGAGGCG  
 1951 CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA  
 2001 GGGGGAGGAC GAGGACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG  
 25 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG  
 2101 GTCCTTGACC CCACTCCGG GTTTCACGTG AACCCCGTGG TGGTGTTCGA  
 30 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCCACAAC CTGTGCTTCA  
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG  
 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC  
 35 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA  
 2351 TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC  
 40 2401 GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACCTCGGT  
 2451 GTACGGGTTTC ACGGGAGCGC AGCACGGACT CCTGCCGTGC CTGCACGTTG  
 2501 CCGCGACGGT GACGACCATC GGCGCGAGA TGCTGCTCGC GACCCGCGAG  
 45 2551 TACGTCCACG CGCGCTGGC GGCCTTCGAA CAGCTCCTGG CCGATTCCCC  
 2601 GGAGGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT  
 50 2651 ACGGGGACAC GGACTCCATA TTTGTGCTGT GCCGCCGCCT CACGGCCGCC  
 2701 GGGCTGACGG CCATGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT  
 2751 GTTTCTGCC CCCATCAAAC TCGAGTGCAG AAAGACGTT ACCAAGCTGC  
 55 2801 TGCTGATCGC CAAGAAAAAG TACATCGCG TCATCTACGG GGGTAAGATG  
 2851 CTCATCAAGG GCGTGGATCT GGTGCGAAA AACAACTGCG CGTTTATCAA

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2901 CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTACGAC GATACCGTAT  
2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG  
5 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC  
3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTCCCTCA  
3101 CCGCCGAACt GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC  
10 3151 CACCTGACGG TGTATTACAA GCTCATGGCC CGCCGCGCGC AGGTCCCGTC  
3201 CATCAAGGAC CGGATCCC GT ACGTGATCGT GGCCCAGACC CGCGAGGTAG  
15 3251 AGGAGACGGT CGCGCGGCTG GCCGCCCTCC GCGAGCTAGA CGCCGCCGCC  
3301 CCAGGGGACG AGCCC GCCCC CCCC CGCGGCC CTGCCCTCCC CGGCCAAGCG  
3351 CCCCCGGGAG ACGCCGTCGC ATGCCGACCC CCCGGGAGGC GCGTCCAAGC  
20 3401 CCCGCAAGCT GCTGGTGTCC GAGCTGGCCG AGGATCCCGC ATACGCCATT  
3451 GCCCACGGCG TCGCCCTGAA CACGGACTAT TACTTCTCCC ACCTGTTGGG  
25 3501 GGC GGCGTGC GTGACATTCA AGGCCCTGTT TGGGAATAAC GCCAAGATCA  
3551 CCGAGAGTCT GTTAAAAAGG TTTATTCCCG AAGTGTGGCA CCCCCCGGAC  
3601 GACGTGGCCG CGCGGCTCCG GGCCGCAGGG TTCGGGGCGG TGGGTGCCGG  
30 3651 CGCTACGGCG GAGGAAACTC GTCGAATGTT GCATAGAGCC TTTGATACTC  
3701 TAGCATGA

35

**SEQ.ID.NO. 6 Amino acid sequence of DNA polymerase for HSV1-KOS-M1**

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPLC RQNFYNPYLA  
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRIAPR VLDEDAPPEK RAGVHDGHLK  
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY  
 10 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAHVYG  
 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA  
 15 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCPAI KKYEGGVDAT  
 301 TRFILDNPFG VTFGWYRLKP GRNNNTLAQPR APMAFGTSSD VEFNCTADNL  
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD  
 20 401 LSTTALEHVL LFSLGSCDLP ESHLNELAAR GLPTPVVLEF DSEFEMLLAF  
 451 MTLVKQYQPE FVTGYNINF DWPFLLAKLT DIYKVPLDGY GRMNGRGVFR  
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVAEAVLKD  
 25 551 KKKDLSYRDI PAYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA  
 601 VARLAGINIT RTIYDGQQIR VFTCLLRLAD QKGFILPDTQ GRFRGAGGEA  
 30 651 PKRPAAARED EERPEEEGED EDEREEGGGE REPEGARETA GRHVGYQGAR  
 701 VLDPTSGFHV NPVVVFDFAS LYPSSIQAHN LCFSTLSLRA DAVAHLLEAGK  
 751 DYLEIEVGGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA  
 35 801 VLLDKQQAAI KVVCNSVYGF TGAQHGLLPC LHVAATVTTI GREMLLATRE  
 851 YVHARWAAFE QLLADFPPEAA DMRAPGPYSM RIYGDTDSI FVLCRGLTAA  
 40 901 GLTAMGDKMA SHISRALFLP PIKLECEKTF TKLLLIAKKK YIGVITYGGKM  
 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAEEWLA  
 1001 RPLPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA  
 45 1051 HLTVYYKLMA RRAQVPSIKD RIPPYVIVAQT REVEETVARL AALRELDAAA  
 1101 PGDEPAPPAA LPSPAKRPRE TPSHADPPGG ASKPRKLLVS ELAEDPAYAI  
 50 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD  
 1201 DVAARLRAAG FGAVGAGATA EETRRMLHRA FDTLA\*

**SEQ.ID.NO. 7 DNA sequence of HSV polymerase gene for HSV1-F-M1**

1 ATGTTTCCG GTGGCGGCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC  
 5 51 CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC  
 10 101 GGGGACCCCC GCCTTGCTTG AGGCAAAACT TTTACAACCC CTACCTCGCC  
 15 151 CCAGTCGGGA CGCAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA  
 20 201 CTATAGCGAA TGCGATGAAT TTCGATTCA CGCCCCGCGG GTGCTGGACG  
 25 251 AGGATGCCCG CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG  
 30 301 CGCGCCCCCA AGGTGTACTG CGGGGGGAC GAGCGCGACG TCCTCCCGT  
 35 351 CGGGTCGGGC GGCTTCTGGC CGCGGCGCTC GCGCCTGTGG GGCGCGTGG  
 40 401 ACCACGCCCGG GGCGGGGTTTC AACCCCACCG TCACCGTCTT TCACGTGTAC  
 45 451 GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCCAGTT  
 50 501 CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC  
 55 551 TCCTGGGCCT GACTCCGGAA GGCCACCGGG TGGCCGTTCA CGTTTACGGC  
 60 601 ACGCGGCAGT ACTTTTACAT GAACAAGGAG GAGGTCGACA GGCACCTACA  
 65 651 ATGCCGCGGCC CCACGAGATC TCTGCGAGCG CATGGCCGCG GCCCTGCGCG  
 70 701 AGTCCCCGGG CGCGTCGTTTC CGCGGCATTT CCGCGGACCA CTTCGAGGCG  
 75 751 GAGGTGGTGG AGCGCACCGA CGTGTACTAC TACGAGACGC GCCCCGCTCT  
 80 801 GTTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGTGTGCG TACCTGTGCG  
 85 851 ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC  
 90 901 ACCCGGTTCA TCCTGGACAA CCCCCGGGTTTC GTCACCTTCG GCTGGTACCG  
 95 951 TCTCAAACCG GGCGGAACA ACACGCTAGC CCAGCCGCGG GCCCCGATGG  
 100 1001 CCTTCGGGAC ATCCAGCGAC GTCGAGTTA ACTGTACGGC GGACAACCTG  
 105 1051 GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT  
 110 1101 CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG  
 115 1151 CGGGGCACCC GGAGGACCTG GTCATCCAGA TATCCTGTCT GCTCTACGAC  
 120 1201 CTGTCCACCA CCGCCCTGGA GCACGTCTC CTGTTTTCGC TCGGTTCCCTG  
 125 1251 CGACCTCCCC GAATCCCACC TGAACGAGCT GGCGGCCAGG GGCCTGCCCA  
 130 1301 CGCCCGTGGT TCTGGAATTG GACAGCGAAT TCGAGATGCT GTTGGCCTTC  
 135 1351 ATGACCCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT  
 140 1401 CATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGCTGACG GACATTACAG  
 145 1451 AGGTCCCCCT GGACGGGTAC GGCGCATGA ACGGCCGGGG CGTGTTCGC  
 150 1501 GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT

	1551	GAACGGCATG GTGAACATCG ACATGTACGG GATTATAACC GACAAGATCA
5	1601	AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC
	1651	AAGAAGAAGG ACCTGAGCTA TCGCGACATC CCCGCCTACT ACGCCGCCGG
	1701	GCCCCGCGCAA CGCGGGGTGA TCGCGAGTA CTGCATACAG GATTCCCTGC
10	1751	TGGTGGGCCA GCTGTTTTT AAGTTTTGC CCCATCTGGA GCTCTGGCC
	1801	GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA
15	1851	GCAGATCCGC GTCTTACGT GCCTGCTGCG CCTGGCCGAC CAGAAGGGCT
	1901	TTATTCTGCC GGACACCCAG GGGCGATTAA GGGGCGGCCGG GGGGGAGGCG
	1951	CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA
20	2001	GGGGGAGGAC GAGGACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG
	2051	AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG
25	2101	GTCCTTGACC CCACTTCCGG GTTTCATGTG AACCCCGTGG TGGTGTTCGA
	2151	CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCCACAAC CTGTGCTTCA
	2201	GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG
30	2251	GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC
	2301	TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTGCCA
	2351	TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC
35	2401	GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACTCGGT
	2451	TTACGGGTTTC ACGGGAGCGC AGCACGGACT CCTGCCGTGC CTGCACGTTG
40	2501	CCGCGACGGT GACGACCATC GGCCGCGAGA TGCTGCTCGC GACCCGCGAG
	2551	TACGTCCACG CGCGCTGGC GGCTTCGAA CAGCTCCTGG CCGATTCCC
45	2601	GGAGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT
	2651	ACGGGGACAC GGACTCCATC TTTGTGCTGT GCCGCGGCCT CACGGCCGCC
	2701	GGGCTGACGG CCGTGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT
50	2751	GTTTCTGTCC CCCATCAAAC TCGAGTGCAGA AAAGACGTTT ACCAAGCTGC
	2801	TGCTGATCGC CAAGAAAAAG TACATCGCG TCATCTACGG GGGTAAGATG
	2851	CTCATCAAGG GCGTGGATCT GGTGCGAAA AACAACTGCG CGTTTATCAA
55	2901	CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTTACGAC GATACCGTAT
	2951	CCGGAGCGGC CGCCGCGTTA GCGAGCGCC CCGCAGAGGA GTGGCTGGCG
60	3001	CGACCCCTGC CCGAGGGACT GCAGGCGTTT GGGGCCGTCC TCGTAGACGC
	3051	CCATCGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTCCCTCA
65	3101	CCGCCGAACG GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC

3151 CACCTGACGG TGTATTACAA GCTCATGGCC CGCCGCGCGC AGGTCCCGTC  
3201 CATCAAGGAC CGGATCCCGT ACGTGATCGT GGCCCAGACC CGCGAGGTAG  
5 3251 AGGAGACGGT CGCGCGGCTG GCCGCCCTCC GCGAGCTCGA CGCCGCCGCC  
3301 CCAGGGGACG AGCCCCCCCC CCCCGCGGCC CTGCCCTCCC CGGCCAAGCG  
10 3351 CCCCCGGGAG ACGCCGTTGC ATGCCGACCC CCCGGGAGGC GCGTCCAAGC  
3401 CCCGCAAGCT GCTGGTGTCC GAGCTGGCCG AGGATCCCGC ATACGCCATT  
3451 GCCCACGGCG TCGCCCTGAA CACGGACTAT TACTTCTCCC ACCTGTTGGG  
15 3501 GGC GGCGTGC GTGACATTCA AGGCCCTGTT TGGGAATAAC GCCAAGATCA  
3551 CCGAGAGTCT GTTAAAAAGG TTTATTCCCG AAGTGTGGCA CCCCCCGGAC  
3601 GACGTGGCCG CGCGGCTCCG GGCCGCAGGG TTCCGGGCGG TGGGTGCCGG  
20 3651 CGCTACGGCG GAGGAAACTC GTCGAATGTT GCATAGAGCC TTTGATACTC  
3701 TAGCATGA

## SEQ.ID.NO. 8 Amino acid sequence of DNA polymerase for HSV1-F-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPLC RQNFYNPYLA  
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRFIAPR VLDEDAPPEK RAGVHDGHLK  
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY  
 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRAVAVHVG  
 201 TRQYFYMNKE EVDRHLQCRA PRDLCEMAA ALRESPGASF RGISADHFEA  
 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCPAI KKYEGGVDAT  
 301 TRFILDNPFG VTFGWYRLKP GRNNNTLAQPR APMAFGTSSD VEFNCTADNL  
 351 AIEGGMSDLP AYKLMLCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD  
 401 LSTTALEHVL LFSLGSCDLP ESHLNELAAR GLPTPVVLEF DSEFEMLLAF  
 451 MTLVKQYQPE FVTGYNINF DWPFLLAKLT DIYKVPLDGY GRMNGRGVFR  
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVAEAVLKD  
 551 KKKDLSYRDI PAYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA  
 601 VARLAGINIT RTIYDGQQIR VFTCLLRLAD QKGFILPDTQ GRFRGGGGEA  
 651 PKRPAAARED EERPEEEGED EDEREEGGGE REPEGARETA GRHVGYQGAR  
 701 VLDPTSGFHV NPVVVFDFAS LYPSSIQAHN LCFSTLSLRA DAVAHLEAGK  
 751 DYLEDIEVGGRLFFFKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA  
 801 VLLDKQQAAI KVVCNSVYGF TGAQHGLLPC LHVAATVTTI GREMLLATRE  
 851 YVHARWAAFE QLLADFPEAA DMRAPGPYSM RITYGDTDSI FVLCRGLTAA  
 901 GLTAVGDKMA SHISRALFLS PIKLECEKTF TKLLLIAKKK YIGVIYGGKM  
 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAEEWLA  
 1001 RPLPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA  
 1051 HLTVYYKLMA RRAQVPSIKD RIPYVIVAQT REVEETVARL AALRELDAAA  
 1101 PGDEPAPPAA LPSPAKRPRE TPLHADPPGG ASKPRKLLVS ELAEDPAYAI  
 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD  
 1201 DVAARLRAAG FGAVGAGATA EETRRMLHRA FDTLA\*

**SEQ.ID.NO. 9** DNA sequence of HSV polymerase gene for HSV1-DJL-M1

1 ATGTTTCCG GTGGCGGCCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC  
 5 51 CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC  
 10 101 GGGGACCCCC GCCTGTGG AGGCAAAACT TTTACAACCC CTACCTCGCC  
 151 CCAGTCGGGA CGAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA  
 10 201 CTATAGCGAA TGCGATGAAT TTCGATTAT CGCCCCGCGG GTGCTGGACG  
 251 AGGATGCCCG CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG  
 15 301 CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCCTCCGCGT  
 351 CGGGTCGGGC GGCTCTGGC CGCGCGCTC GGCCTGTGG GGCGGCGTGG  
 401 ACCACGCCCG GGCGGGGTTTC AACCCCCACCG TCACCGTCTT TCACGTGTAT  
 20 451 GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCAGTT  
 501 CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC  
 25 551 TCCTGGGCCT GACTCCGGAA GGCCACCGGG TGGCCGTTCA CGTTACGGC  
 601 ACGCGGCAGT ACTTTACAT GAACAAGGAG GAGGTTGACA GGCACCTACA  
 651 ATGCCCGGCC CCACGAGATC TCTGCGAGCG CATGCCGCG GCCCTGCGCG  
 30 701 AGTCCCCGGG CGCGTCGTTT CGCGGCATCT CCGCGGACCA CTTCGAGGCG  
 751 GAGGTGGTGG AGCGCACCGA CGTGTACTAC TACGAGACGC GCCCCGCTCT  
 35 801 GTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTCG TACCTGTGCG  
 851 ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC  
 901 ACCCGGTTCA TCCTGGACAA CCCGGGGTTTC GTCACCTTCG GCTGGTACCG  
 40 951 TCTCAAACCG GGCGGAACA ACACGCTAGC CCAGCGCGG GCCCGATGG  
 1001 CCTTCGGGAC ATCCAGCGAT GTCGAGTTA ACTGTACGGC GGACAACCTG  
 45 1051 GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT  
 1101 CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG  
 1151 CGGGGCACCC GGAGGACCTG GTCATCCAGA TATCCTGTCT GCTCTACGAC  
 50 1201 CTGTCCACCA CCGCCCTGGA GCACGTCCCTC CTGTTTCGC TCGGTTCTG  
 1251 CGACCTCCCC GAATCCCACC TGAACGAGCT GGCGGCCAGG GGCGTGCCTA  
 55 1301 CGCCCGTGGT TCTGGAATTG GACAGCGAAT TCGAGATGCT GTTGGCCTTC  
 1351 ATGACCCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT

1401 AATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGCTGACG GACATTACA  
 1451 AGGTCCCCCT GGACGGGTAC GGCGCATGA ACGGCCGGGG CGTGTTCGC  
 5 1501 GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT  
 1551 GAACGGCATG GTGAACATCG ACATGTACGG GATTATAACC GACAAGATCA  
 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CGAAGCCGT CCTGAAGGAC  
 10 1651 AAGAAGAAGG ACCTGAGCTA TCGCGACATC CCCACCTACT ACGCCGCCGG  
 1701 GCCCGCGCAA CGCGGGGTGA TCGCGAGTA CTGCATACAG GATTCCCTGC  
 15 1751 TGGTGGGCCA GCTGTTTTT AAGTTTTGC CCCATCTGGA GCTCTGGCC  
 1801 GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA  
 1851 GCAGATCCGC GTCTTACGT GCCTGCTGGC CCTGGCCGAC CAGAAGGGCT  
 20 1901 TTATTCTGCC GGACACCCAG GGGCGATTAA GGGGCGCCGG GGGGGAGGCG  
 1951 CCCAAGCGTC CGGCCGCAGC CCAGGAGGAC GAGGAGCGGC CAGAGGAGGA  
 25 2001 GGGGGAGGAC GAGAACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG  
 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG  
 2101 GTCCTTGACC CCACTTCCGG GTTTCACGTG AACCCCGTGG TGGTGTTCGA  
 30 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCCACAAC CTGTGCTTCA  
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG  
 35 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC  
 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA  
 2351 TGCAGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC  
 40 2401 GTGCTCCTGG ACAAGCAGCA GGCGGCCATC AAGGTCGTGT GTAACCTCGGT  
 2451 TTACGGGTTACGGAGCGC AGCACGGACT CCTGCCGTGC CTGCACGTTG  
 45 2501 CCGCGACGGT GACGACCATC GGCGCGAGA TGCTGCTCGC GACCCCGAG  
 2551 TACGTCCACG CGCGCTGGC GGCTTCGAA CAGCTCCTGG CCGATTCCCC  
 2601 GGAGGCAGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT  
 50 2651 ACGGGGACAC GGACTCCATA TTTGTGCTGT GCCGCGGCCCT CACGGCCGCC  
 2701 GGGCTGACGG CCGTGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT  
 55 2751 GTTCTGCC CCCATCAAAC TCGAGTGCAG AAAGACGTTCA ACCAAGCTGC  
 2801 TGCTGATCGC CAAGAAAAAG TACATCGCGC TCATCTACGG GGGTAAGATG  
 2851 CTCATCAAGG GCGTGGATCT GGTGCGAAA AACAACTGCG CGTTTATCAA

2901 CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTACGAC GATACCGTAT  
2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG  
5 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC  
3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTTCTCA  
10 3101 CCGCCGAACt GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC  
3151 CACCTGACGG TGTATTACAA GCTCATGGCC CGCCGCGCGC AGGTCCC GT  
15 3201 CATCAAGGAC CGGATCCC GT ACGTGATCGT GGCCCAGACC CGCGAGGTAG  
3251 AGGAGACGGT CGCGCGGCTG GCCGCCCTCC GCGAGCTAGA CGCCGCCG  
3301 CCAGGGGACG AGCCGCC CCCCCGCGGCC CTGCCCTCCC CGGCCAAGCG  
20 3351 CCCCCGGGAG ACGCCGTCGC CTGCCGACCC CCCGGGAGGC GCGTCCAAGC  
3401 CCCGCAAGCT GCTGGTGTCC GAGCTGGCCG AGGATCCC GC ATACGCCATT  
3451 GCCCACGGCG TCGCCCTGAA CACGGACTAT TACTTCTCCC ACCTGTTGGG  
25 3501 GGCGCGTGC GTGACATTCA AGGCCCTGTT TGGGAATAAC GCCAAGATCA  
3551 CCGAGAGTCT GTTAAAAAGG TTTATTCCCG AAGTGTGGCA CCCCCCGGAC  
30 3601 GACGTGGCCG CGCGGCTCCG GACCGCAGGG TTCGGGGCGG TGGGTGCCGG  
3651 CGCTACGGCG GAGGAAACTC GTCGAATGTT GCATAGAGCC TTTGATACTC  
3701 TAGCATGA  
35

## SEQ.ID.NO. 10 Amino acid sequence of DNA polymerase for HSV1-DJL-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPL RQNFYNPYLA  
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRFIAPR VLDEDAPPEK RAGVHDGHLK  
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY  
 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAVHVYG  
 10 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA  
 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCPAI KKYEGGVDAT  
 15 301 TRFILDNPFGF VTFGWYRLKP GRNNNTLAQPR APMAFGTSSD VEFNCTADNL  
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD  
 401 LSTTALEHVL LFSLGSCDLP ESHLNELAAR GLPTPVVLEF DSEFEMLLAF  
 20 451 MTLVKQYGPE FVTGYNINF DWPFLLAKLT DIYKVPLDGY GRMNGRGVFR  
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVAЕAVLKD  
 25 551 KKKDLSYRDI PTYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA  
 601 VARLAGINIT RTIYDGQQIR VFTCLLRLAD QKGFILPDTQ GRFRGAGGEA  
 651 PKRPAAARED EERPEEEGED ENEREEGGGE REPEGARETA GRHVGYQGAR  
 30 701 VLDPTSGFHV NPVVVFDFAS LYPSSIQAHN LCFSTLSLRA DAVAHEAGK  
 751 DYLEDVGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA  
 35 801 VLLDKQQAAI KVVCNSVYGF TGAQHGLLPC LHVAATVTTI GREMLLATRE  
 851 YVHARWAAFE QLLADFPEAA DMRAPGPYSM RIYGDTSI FVLCRGLTAA  
 901 GLTAVGDKMA SHISRALFLP PIKLECEKTF TKLLLIAKKK YIGVITYGGKM  
 40 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAEEWLA  
 1001 RPLPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA  
 45 1051 HLTVYYKLMA RRAQVPSIKD RIPYVIVAQT REVEETVARL AALRELDAAA  
 1101 PGDEPAPPAA LPSPAKRPRE TPSPADPPGG ASKPRKLLVS ELAEDPAYAI  
 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD  
 50 1201 DVAARLRTAG FGAVGAGATA EETRRMLHRA FDTLA\*

**SEQ.ID.NO. 11 DNA sequence of DNA polymerase gene for HMCV-AD169-M1**

1 ATGTTTTCA ACCCGTATCT GAGCGGCCGG GTGACCGGCG GTGCGGTCGC  
 5 51 GGGTGGCCGG CGTCAGCGTT CGCAGCCGG CTCCGCGCAG GGCTCGGGCA  
 10 101 AGCGGCCGCC ACAGAAACAG TTTTGAGA TCGTCCGCG AGGTGTCATG  
 151 TTCGACGGTC AGACGGGTT GATCAAGCAT AAGACGGGAC GGCTGCCTCT  
 10 201 CATGTTCTAT CGAGAGATTA AACATTGTT GAGTCATGAC ATGGTTTGGC  
 251 CGTGTCCCTTG GCGCGAGACC CTGGTGGTC GCGTGGTGGG ACCTATTCGT  
 15 301 TTTCACACCT ACGATCAGAC GGACGCCGTG CTCTCTTCG ACTCGCCGA  
 351 AAACGTGTCG CCGCGCTATC GTCAGCATCT GGTGCCCTCG GGGAACGTGT  
 401 TGCGTTCTT CGGGGCCACA GAACACGGCT ACAGTATCTG CGTCAACGTT  
 20 451 TTCGGGCAGC GCAGCTACTT TTACTGTGAG TACAGCGACA CCGATAAGGCT  
 501 GCGTGAGGTC ATTGCCAGCG TGGCGAAGT AGTGCCCGAA CCGCGGACGC  
 25 551 CATA CGCCGT GTCTGTCACG CCGGCCACCA AGACCTCCAT CTATGGGTAC  
 601 GGGACCGCAGC CCGTGCCCCGA TTTGCAGTGT GTGTCTATCA GCAACTGGAC  
 651 CATGCCAGA AAAATCGGCG AGTATCTGCT GGAGCAGGGT TTTCCCGTGT  
 30 701 ACGAGGTCCG TGTGGATCCG CTGACCGT TGGTCATCGA TCGGCGGATC  
 751 ACCACGTTCG GCTGGTGCTC CGTGAATCGT TACGACTGGC GGCAGCAGGG  
 35 801 TCGCGCGTCG ACTTGTGATA TCGAGGTAGA CTGCGATGTC TCTGACCTGG  
 851 TGGCTGTGCC CGACGACAGC TCGTGGCCGC GCTATCGATG CCTGTCCCTC  
 901 GATATCGAGT GCATGAGCGG CGAGGGTGGT TTTCCCTGCG CCGAGAACGTC  
 40 951 CGATGACATT GTCATTCAA TCTCGTGCCT GTGCTACGAG ACGGGGGGAA  
 1001 ACACCGCCGT GGATCAGGGG ATCCCAAACG GGAACGATGG TCGGGGCTGC  
 45 1051 ACTTCGGAGG GTGTGATCTT TGGGCACTCG GGTCTTCATC TCTTACGAT  
 1101 CGGCACCTGC GGGCAGGTGG GCCCAGACGT GGACGTCTAC GAGTTCCCTT  
 1151 CCGAATACGA GCTGCTGCTG GGCTTATGC TTTCTTCA ACGGTACGCG  
 50 1201 CGGGCCTTG TGACCGGTTA CAACATCAAC TCTTTGACT TGAAGTACAT  
 1251 CCTCACGCGT CTCGAGTACC TGTATAAGGT GGACTCGCAG CGCTTCTGCA  
 55 1301 AGTTGCCTAC GGCGCAGGGC GGCGTTCT TTTACACAG CCCCGCCGTG  
 1351 GGTTTAAGC GGCAGTACGC CGCCGCTTT CCCTCGGCTT CTCACAACAA

1401 TCCGGCCAGC ACGGCCGCCA CCAAGGTGTA TATTGCGGGT TCGGTGGTTA  
 1451 TCGACATGTA CCCTGTATGC ATGGCCAAGA CTAACTCGCC CAACTATAAG  
 5 1501 CTCAACACTA TGGCCGAGCT TTACCTGCGG CAACGCAAGG ATGACCTGTC  
 1551 TTACAAGGAC ATCCCGCGTT GTTTCGTGGC TAATGCCAG GGC CGCGCCC  
 1601 AGGTAGGCCG TTACTGTCTG CAGGACGCCG TATTGGTGCG CGATCTGTTC  
 10 1651 AACACCATTA ATTTCACTA CGAGGCCGGG GCCATCGCGC GGCTGGCTAA  
 1701 AATTCCGTTG CGGCGTGTCA TCTTGACGG ACAGCAGATC CGTATCTACA  
 15 1751 CCTCGCTGCT GGACGAGTGC GCCTGCCCGC ATTTATCCT GCCCAACCAC  
 1801 TACAGCAAAG GTACGACGGT GCCCGAAACG AATAGCGTTG CTGTGTCACC  
 1851 TAACGCTGCT ATCATCTCTA CCGCCGCTGT GCCCGGCGAC GCGGGTTCTG  
 20 1901 TGGCGGCTAT GTTCAGATG TCGCCGCCCT TGCAATCTGC GCCGTCCAGT  
 1951 CAGGACGGCG TTTCACCCGG CTCCGGCAGT AACAGTAGTA GCAGCGTCGG  
 25 2001 CGTTTCAGC GTCGGCTCCG GCAGTAGTGG CGCGTCCGG GTTTCCAACG  
 2051 ACAATCACGG CGCCGGCGGT ACTGCGGCCGG TTTCGTACCA GGGCGCCACG  
 2101 GTGTTTGAGC CCGAGGTGGG TTACTACAAC GACCCCGTGG CCGTGGTCA  
 30 2151 CTTTGCCAGC CTCTACCCCT CCATCATCAT GGCCCACAAC CTCTGCTACT  
 2201 CCACCTGCT GGTGCCGGGT GGCGAGTACC CTGTGGACCC CGCGACGTA  
 2251 TACAGCGTCA CGCTAGAGAA CGCGTGACC CACCGCTTG TCGTGCTTC  
 2301 GGTGCGCGTC TCGGTGCTCT CGGAACGTGCT CAACAAGTGG GTTTGCAGC  
 2351 GGCGTGCCTG GCGCGAATGC ATGCGCGAGT GTCAAGACCC TGTGCCCGT  
 40 2401 ATGCTGCTCG ACAAGGAACA GATGGCGCTC AAAGTAACGT GCAACGCTTT  
 2451 CTACGGTTTT ACCGGCGCGC TGAACGGTAT GATGCCGTGT CTGCCCATCG  
 45 2501 CCGCCAGCAT CACGCGCATC GGTCGCGACA TGCTAGAGCG CACGGCGCGG  
 2551 TTCATCAAAG ACAACTTTTC AGAGCCGTGT TTTTGACAA ATTGTTTAA  
 2601 TCAGGAAGAC TATGTAGTGG GAACGCGGGA GGGGGATTG GAGGAGAGCA  
 50 2651 GCGCGTTACC GGAGGGGCTC GAAACATCGT CAGGGGGCTC GAACGAACGG  
 2701 CGGGTGGAGG CGCGGGTCAT CTACGGGGAC ACGGACAGCG TGTTGTCCG  
 2751 CTTTCGTGGC CTGACGCCGC AGGCTCTGGT GGCGCGTGGG CCCAGCCTGG  
 2801 CGCACTACGT GACGGCCTGT CTTTTGTGG AGCCCGTCAA GCTGGAGTTT  
 2851 GAAAAGGTCT TCGTCTCTCT TATGATGATC TGCAAGAAC GTTACATCGG

2901 CAAAGTGGAG GGCGCCTCGG GTCTGAGCAT GAAGGGCGTG GATCTGGTGC  
2951 GCAAGACGGC CTGCGAGTTC GTCAAGGGCG TCACCGTGA CGTCCTCTCG  
5  
3001 CTGCTCTTG AGGATCGCGA GGTCTCGGAA GCAGCCGTGC GCCTGTCGCG  
3051 CCTCTCACTC GATGAAGTCA AGAAGTACGG CGTGCCACGC GGTTTCTGGC  
10  
3101 GTATCTTACG CCGCTTGGTG CAGGCCCGCG ACGATCTGTA CCTGCACCGT  
3151 GTGCGTGTGCG AGGACCTGGT GCTTTCGTGCG GTGCTCTCTA AGGACATCTC  
3201 GCTGTACCGT CAATCTAACCG TGCCGCACAT TGCCGTATT AAGCGATTGG  
15  
3251 CGGCCCGTTC TGAGGAGCTA CCCTCGGTGCG GGGATCGGGT CTTTACGTT  
3301 CTGACGGCGC CCGGTGTCCG GACGGCGCCG CAGGGTTCCCT CCGACAACGG  
20  
3351 TGATTCTGTA ACCGCCGGCG TGTTTCCCG GTCGGACGCG ATTGATGGCA  
3401 CGGACGACGA CGCTGACGGC GGCGGGGTAG AGGAGAGCAA CAGGAGAGGA  
3451 GGAGAGCCGG CAAAGAAGAG GGCGCGGAAA CCACCGTCGG CCGTGTGCAA  
25  
3501 CTACGAGGTA GCCGAAGATC CGAGCTACGT GCGCGAGCAC GGCGTGCCA  
3551 TTCACGCCGA CAAGTACTTT GAGCAGGTTTC TCAAGGCTGT AACTAACGTG  
30  
3601 CTGTCGCCCCG TCTTCCCAGG CGCGAAACC GCGCGCAAGG ACAAGTTTT  
3651 GCACATGGTG CTGCCGCCGC GCTTGCACCT GGAGCCGGCT TTTCTGCCGT  
35  
3701 ACAGTGTCAA GGCGCACGAA TGCTGTTGA

**SEQ. ID. NO. 12 Amino acid sequence of DNA polymerase for HCMV-AD169-M1**

1 MFFNPYLSGG VTGGAVAGGR RQRSQPGSAQ GSGKRPPQKQ FLQIVPRGVM  
 5 51 FDGQTGLIKH KTGRPLLMFY REIKHLLSHD MVWPCPWRET LVGRVVGP  
 101 FHTYDQTDAT LFFDSPENVS PRYRQHLVPS GNVLRFQGAT EHGYSCVNV  
 10 151 FGQRSYFYCE YSDTDRLREV IASVGELVPE PRTPYAVSVT PAKTSIYGY  
 201 GTRPVPDLQC VSISNWTMAR KIGEYLLEQG FPVYEVRVDP LTRLVIDRRI  
 251 TTFGWCSVNR YDWRQQGRAS TCDIEVDCDV SDLVAVPDDS SWPRYRCLSF  
 15 301 DIECMSGEgg FPCAEKSDDI VIQISCVCYE TGGNTAVDQG IPNGNDGRGC  
 351 TSEGVIFGHS GLHLFTIGTC GQVGPDVDVY EFPSEYELL GFMLFFQRYA  
 20 401 PAFVTGYNIN SFDLKYILTR LEYLYKVDSQ RFCKLPTAQG GRFFLHSPAV  
 451 GFKRQYAAAF PSASHNNPAS TAATKVYIAG SVVIDMYPVC MAKTNSPNYK  
 501 LNTMAELYLR QRKDDLSYKD IPRCFVANAE GRAQVGRYCL QDAVLVRDLF  
 25 551 NTINFHYEAG AIARLAKIPL RRVIFDGQQI RIYTSLLDEC ACRDFILPNH  
 601 YSKGTTVPET NSVAVSPNAA IISTAAVPGD AGSVAAMFQM SPPLQSAPSS  
 30 651 QDGVS PGSGS NSSSSVGVFS VGSGSSGGVG VSNDNHGAGG TAAVSYQGAT  
 701 VFEPEVGYYN DPVAVFDFAS LYPsiIMAHN LCYSTLLVPG GEYPVDPADV  
 751 YSVTLENGVT HRFVRASVRV SVLSELLNKW VSQRRAVREC MRECQDPVRR  
 35 801 MLLDKEQMAL KVTCNAFYGF TGALNGMMPC LPIAASITRI GRDMLERTAR  
 851 FIKDNFSEPC FLHNFFNQED YVVGTRREGDS EESSALPEG ETSSGGSNER  
 40 901 RVEARVITYGD TDSVFVFRG LTPQALVARG PSLAHYVTAC LFVEPVKLEF  
 951 EKVFVSLMMI CKKRYIGKVE GASGLSMKGV DLVRKTACEF VKGVTRDVLS  
 1001 LLFEDREVSE AAVRLSRLSL DEVKKYGVPR GFWRILRRLV QARDDLYLHR  
 45 1051 VRVEDLVLSS VLSKDISLYR QSNLPHIAVI KRLAARSEEL PSVGDRVFYV  
 1101 LTAPGVRTAP QGSSDNGDSV TAGVVSRSDA IDGTDDDADG GGVEESNRRG  
 50 1151 GEPAKKRARK PPSAVCNYEV AEDPSYVREH GVPIHADKYF EQVLKAVTNV  
 1201 LSPVFFPGGET ARKDKFLHMV LPRLHLEPA FLPYSVKAHE CC\*

**Figure 6**  
**SEQ.ID.NO.13 Amino acid sequence of DNA polymerase for HCMV-AD169**

5        1 MFFNPYLSGG VTGGAVAGGR QRQSQPGSAQ GSGKRPPQKQ FLQIVPRGVM  
 51      51 FDGQTGLIKH KTGRPLPLMFY REIKHLLSHD MVWPCPWRET LVGRVVGPIR  
 10     101 FHTYDQTDAT LFFDSPENVS PRYRQHLVPS GNVLRFFGAT EHGYSCIVNV  
 10     151 FGQRSYFYCE YSDTDRRLREV IASVGELVPE PRTPYAVSVT PATKTSIYGY  
 15     201 GTRPVPDLC VSIISNWTMAR KIGEYLLEQG FPVYEVRVDP LTRLVIDRRI  
 15     251 TTFGWCSVNR YDWRQQGRAS TCDIEVDCDV SDLVAVPDDS SWPRYRCLSF  
 20     301 DIECMSGEgg FFPCAEKSDDI VIQISCVCYE TGGNTAVDQG IPNGNDGRGC  
 20     351 TSEGVIIFGHS GLHLFTIGTC GQVGPDVDVY EFPSEYELL GFMLFFQRYA  
 20     401 PAFVTGYNIN SFDLKYLTR LEYLYKVDSQ RFCKLPTAQG GRFFLHSPAV  
 25     451 GFKRQYAAAF PSASHNNPAS TAATKVYIAG SVVIDMYPVC MAKTNSPNYK  
 25     501 LNTMAELYLR QRKDDLSYKD IPRCFVANAE GRAQVGRYCL QDAVLVRDLF  
 25     551 NTINFHYEAG AIARLAKIPL RRVIFDGQQI RIYTSLLDEC ACRDFILPNH  
 30     601 YSKGTTVPET NSVAVSPNAA IISTAAVPGD AGSVAAMFQM SPPLQSAPSS  
 30     651 QDGVSPGSGS NSSSSVGVFS VGSGSSGGVG VSNDNHGAGG TAAVSYQGAT  
 35     701 VFEPEVGYYN DPVAVFDFAS LYPSIIMAHN LCYSTLLVPG GEYPVDPADV  
 35     751 YSVTLENGVT HRFVRASRVV SVLSELLNKW VSQRRAVREC MRECQDPVRR  
 40     801 MLLDKEQMAL KVTCNAFYGF TGVVNGMMPC LPIAASITRI GRDMLERTAR  
 40     851 FIKDNFSEPC FLHNFFNQED YVVGTRREGDS EESSALPEG ETSSGGSNER  
 40     901 RVEARVIYGD TDSVFVRFRG LTPQALVARG PSLAHYVTAC LFVEPVKLEF  
 45     951 EKVFVSLMMI CKKRYIGKVE GASGLSMKGKV DLVRKTACEF VKGVTRDVLS  
 45     1001 LLFEDREVSE AAVRLSRLSL DEVKKYGVPR GFWRILRRLV QARDDLYLHR  
 50     1051 VRVEDLVLSS VLSKDISLYR QSNLPHIAVI KRLAARSEEL PSVGDRVFYV  
 50     1101 LTAPGVRTAP QGSSDNGDSV TAGVVSRSDA IDGTDDDADG GGVEESNRRG  
 50     1151 GEPACKRARK PPSAVCNYEV AEDPSYVREH GVPIHADKYF EQVLKAVTNV  
 55     1201 LSPVFPGET ARKDKFLHMV LPRLHLEPA FLPYSVKAHE CC\*

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